



SEQUENCE LISTING

<110> Duvick, Jonathan P.
Gilliam, Jacob T.
Maddox, Joyce R.
Rao, Aragula Gururaj
Crasta, Oswald R.
Folkerts, Otto

<120> Amino Polyol Amine Oxidase
Polynucleotides and Related Polypeptides and Methods of Use

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<150> US 60/093,936
<151> 1998-07-25

<150> US 60/135,391
<151> 1999-05-21

<150> US 09/352,159
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tgctatagta	ccccaggata	gaatttccg	ccaatgcttg	cttctcgccg	ggaagaggtg	300
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gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly 35 40 45	144
ccc ggc aya acg act atc aac gac stc ggc gct gcg tgg atc aat gac Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp 50 55 60	192
agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu 65 70 75 80	240
ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac	288

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ggt aca acc act aca gct tat ggt gac tcc ttg ctg agc gag gag			336
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu			
100	105	110	
gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc			384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile			
115	120	125	
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Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg			
130	135	140	
ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg			480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu			
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Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly			
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Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys			
180	185	190	
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg			624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly			
195	200	205	
cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc atg			672
Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met			
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Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala			
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245	250	255	
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260	265	270	
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305	310	315	320

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115	120	125
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg		
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Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu		
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Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly		
165	170	175
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys		
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Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly		
195	200	205
Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met		
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225	230	235
Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly		
245	250	255
Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu		
260	265	270
Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala		
275	280	285
Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val		
290	295	300
Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln		
305	310	315
Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val		
325	330	335
Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg		
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Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp		
355	360	365
Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro		
370	375	380
Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly		
385	390	395
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser		
405	410	415
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr		
420	425	430
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<213> Exophiala spinifera

<220>

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gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly 35 40 45	144
ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp 50 55 60	192
agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu 65 70 75 80	240
ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp 85 90 95	288
ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu 100 105 110	336
gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile 115 120 125	384
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg 130 135 140	432
ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu 145 150 155 160	480
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gtg gaa gcc cac gag atc agc atg ctt ttc ctc acc gac tac atc aag Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys 180 185 190	576
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly 195 200 205	624
cag tat gtg cga tgc aaa aca g gtgcgtgtgg tgcgtctca ggtggggac Gln Tyr Val Arg Cys Lys Thr	676

210

215

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att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala 245 250 255		824
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr Leu Tyr 260 265 270		872
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu 275 280 285		920
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ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala 405 410 415		1304
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag aag tct Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser 420 425 430		1352

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Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg		
435	440	445
ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag		1442
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35 40 45		
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp		
50 55 60		
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu		
65 70 75 80		
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp		
85 90 95		
Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu		
100 105 110		
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile		
115 120 125		
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg		
130 135 140		
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu		
145 150 155 160		
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly		
165 170 175		
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys		
180 185 190		
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly		
195 200 205		
Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met		
210 215 220		
Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala		
225 230 235 240		
Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly		
245 250 255		
Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu		
260 265 270		
Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala		
275 280 285		
Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val		
290 295 300		
Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln		
305 310 315 320		
Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val		
325 330 335		
Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg		

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Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro		
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Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly		
385	390	395
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser		
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Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr		
420	425	430
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln		
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Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala		
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Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp		
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Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp		
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Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu		
100	105	110
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile		
115	120	125
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg		
130	135	140
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu		
145	150	155
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly		
165	170	175
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys		
180	185	190
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly		
195	200	205
Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly		
210	215	220
Gly Leu Val Ser Gln Trp Ser Phe Gln Val Cys Ser Arg Phe Ala Met		
225	230	235
Pro Cys Gln Arg Asn Leu Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro		
245	250	255
Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro		
260	265	270
Arg Ala Pro Cys Ser Glu Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln		
275	280	285

Pro Cys Ile Pro Pro His His Leu Phe Pro Pro Arg Ser Lys
 290 295 300
 His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr
 305 310 315 320
 Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn
 325 330 335
 Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser
 340 345 350
 Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly
 355 360 365
 Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr
 370 375 380
 Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg
 385 390 395 400
 Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu
 405 410 415
 Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg
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 <212> DNA
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 <223> Extra lysine in K:trAPAO

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ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg	144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
35 40 45	

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat	192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50 55 60	

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg	240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
65 70 75 80	

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa	288
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gac ggt aca acc act aca gct tat ggt gac tcc ttg ctg agc gag															336	
Asp	Gly	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu		
100					105						110					
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg															384	
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	
115					120						125					
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag															432	
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	
130					135					140						
cg g ctc gac agt gtg agc ttc gc g cac tac tgt gag aag gaa cta aac															480	
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Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	
195					200					205						
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Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	
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Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	
225					230				235				240			
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Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	
245					250					255						
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc															816	
Gly	Ala	Val	Phe	Arg	Ser	Lys	V a l	V a l	V a l	Ser	Leu	Pro	Thr	Thr		
260					265					270						
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa															864	
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	
275					280					285						
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata qtc ttc															912	
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	V a l	Phe	
290					295					300						
gta tgg gac aag c g tgg tgg cgc gaa c a ggc ttc tcg ggc qtc ctc															960	
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	V a l	Leu	

305	310	315	320	
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc acc agc atc gac Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325		330		1008
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 340		345		1056
cg ^g aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 355		360		1104
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 370		375		1152
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 385		390		1200
gga qct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 405		410		1248
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu 420		425		1296
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly 435		440		1344
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala 450		455		1389
460				
tag				1392
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Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly 1		5		15
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val 20		25		30
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser 35		40		45
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 50		55		60
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 65		70		80
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln 85		90		95
		12		

Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 100 105 110
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 115 120 125
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 130 135 140
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 145 150 155 160
 Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
 165 170 175
 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
 180 185 190
 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
 195 200 205
 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
 210 215 220
 Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
 225 230 235 240
 Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
 245 250 255
 Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
 260 265 270
 Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
 275 280 285
 Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
 290 295 300
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
 305 310 315 320
 Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
 325 330 335
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 340 345 350
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 355 360 365
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 370 375 380
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 385 390 395 400
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
 405 410 415
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 420 425 430
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 435 440 445
 Gln Arg Gly Aia Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 1:

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence designed for cloning DNA into
expression vectors, N23256

<400> 12

gggaaattca aagacaacgt tgccggacgtg gtag	34	
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<220>		
<223> Primer sequence designed for cloning DNA into expression vectors, N23259		
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ggggcggccg cctatgctgc tggcaccagg ctag	34	
<210> 14		
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<212> DNA		
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<223> Designed oligonucleotide for 3' RACE, N21965		
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tggtttcgtt accgacaacc ttgtatccc	29	
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<212> DNA		
<213> Artificial Sequence		
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gagtttgtcc cagacagact ttgtatccc	28	
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<223> yeast alpha mating factor secretion signal.		
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<232> (1)...(1662)		
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atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc	48	
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser		
-85	-80	-75
gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa	96	
Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln		
-70	-65	-60

att ccg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe -55 -50 -45	144
gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu -40 -35 -30	192
ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val -25 -20 -15 -10	240
tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala -5 1 5	288
gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg 10 15 20	336
aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp 25 30 35	384
cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr 40 45 50 55	432
act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser 60 65 70	480
gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln 75 80 85	528
agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr 90 95 100	576
aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala 105 110 115	624
ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser 120 125 130 135	672
ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val 140 145 150	720
agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu 155 160 165	768
ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa ggc cac 15	816

Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His			
170	175	180	
gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt			864
Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly			
185	190	195	
ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga			912
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg			
200	205	210	215
tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt			960
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu			
220	225	230	
gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag			1008
Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln			
235	240	245	
tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtc ttc cga			1056
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg			
250	255	260	
agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg			1104
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu			
265	270	275	
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat			1152
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn			
280	285	290	295
tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg			1200
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro			
300	305	310	
tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac			1248
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp			
315	320	325	
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg			1296
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp			
330	335	340	
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa			1344
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln			
345	350	355	
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca			1392
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala			
360	365	370	375
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc			1440
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu			
380	385	390	
gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc			1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala			
395	400	405	

gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg		1536	
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr			
410	415	420	
ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg		1584	
Pro Phe Lys Ser Val His Phe Val Gly Thr Ser Leu Val Trp			
425	430	435	
aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca		1632	
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala			
440	445	450	455
gaa gtt gtg gct agc ctg gtg cca gca gca taggcggccg c		1673	
Glu Val Val Ala Ser Leu Val Pro Ala Ala			
460	465		
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<213> Exophiala spinifera			
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Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln			
-70	-65	-60	
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe			
-55	-50	-45	
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu			
-40	-35	-30	
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val			
-25	-20	-15	-10
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala			
-5	1	5	
Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg			
10	15	20	
Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp			
25	30	35	
Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr			
40	45	50	55
Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser			
60	65	70	
Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln			
75	80	85	
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr			
90	95	100	
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala			
105	110	115	
Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser			
120	125	130	135
Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val			
140	145	150	

Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu
 155 160 165
 Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His
 170 175 180
 Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly
 185 190 195
 Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg
 200 205 210 215
 Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu
 220 225 230
 Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln
 235 240 245
 Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg
 250 255 260
 Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu
 265 270 275
 Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn
 280 285 290 295
 Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro
 300 305 310
 Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp
 315 320 325
 Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp
 330 335 340
 Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln
 345 350 355
 Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala
 360 365 370 375
 Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu
 380 385 390
 Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala
 395 400 405
 Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr
 410 415 420
 Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp
 425 430 435
 Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
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 Glu Val Val Ala Ser Leu Val Pro Ala Ala
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<210> 18
 <211> 2079
 <212> DNA
 <213> Unknown

<220>
 <223> GST:K:trAPAO 2079 nt. Translation starting at nt 1
 - 687, gst fusion + polylinker, 688-2076,
 K:trAPAO, extra lysine underlined; 2077-2079, stop
 codon. For bacterial expression.

<231> CDS
 <232> (1)...(2076)

 <231> misc_feature
 <232> (1)...(687)

<223> gst fusion + polylinker

<221> misc_feature

<222> (688)...(2076)

<223> K:trAPAO

<221> misc_feature

<222> (688)...(690)

<223> Extra lysine

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Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
1 5 10 15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg 96
Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
20 25 30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg 144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
35 40 45

ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa 192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60

tta aca cag ttt atg gcc atc ata cgt tat ata gct gac aag cac aac 240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa 288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95

gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt 336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110

aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa 384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125

atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat 432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140

ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat 480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160

gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta 528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175

gtt tgt ttt aia aaa cgt att gaa gct atc cca caa att gat aag tac 576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190

ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala 195	200	205	624
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg 210	215	220	672
gga tcc ccg gaa ttc aaa gac aac gtt gcg gac gtg gta gtg gtg ggc Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly 225	230	235	240
gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly 245	250	255	768
ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr 260	265	270	816
ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly 275	280	285	864
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe 290	295	300	912
gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser 305	310	315	320
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp 325	330	335	1008
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro 340	345	350	1056
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg Val Trp Ser Gln Leu Ile Glu His Ser Leu Gln Asp Leu Lys Ala 355	360	365	1104
agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys 370	375	380	1153
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile 385	390	395	400
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe 405	410	415	1248
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg 20			1296

Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser			
420	425	430	
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag			1344
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln			
435	440	445	
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac			1392
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His			
450	455	460	
ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca			1440
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr			
465	470	475	480
gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt			1488
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val			
485	490	495	
tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt			1536
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu			
500	505	510	
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat			1584
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr			
515	520	525	
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc			1632
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly			
530	535	540	
tcc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga			1680
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg			
545	550	555	560
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg			1728
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met			
565	570	575	
gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga			1776
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg			
580	585	590	
caa aag tct gtc tgg gac caa ctc ccg gca gcc tac gag aac gcc ggg			1824
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly			
595	600	605	
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag			1872
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys			
610	615	620	
cag cag tat ttc caa gga gct ccg aac gcc gtc tat ggg ctg aac gat			1920
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp			
625	630	635	640
ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat			1968
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His			
645	650	655	

ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg		2016
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly		
660	665	670
 gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg		2064
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu		
675	680	685
 gtg cca gca gca tag		2079
Val Pro Ala Ala		
690		
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1 5 10 15		
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20 25 30		
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu		
35 40 45		
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys		
50 55 60		
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn		
65 70 75 80		
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu		
85 90 95		
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser		
100 105 110		
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu		
115 120 125		
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn		
130 135 140		
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp		
145 150 155 160		
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu		
165 170 175		
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr		
180 185 190		
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala		
195 200 205		
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg		
210 215 220		
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly		
225 230 235 240		
Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly		
245 250 255		
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr		
260 265 270		
Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly		
275 280 285		
Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe		
290 295 300		

Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser
 305 310 315 320
 Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp
 325 330 335
 Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro
 340 345 350
 Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala
 355 360 365
 Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys
 370 375 380
 Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile
 385 390 395 400
 Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe
 405 410 415
 Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser
 420 425 430
 Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln
 435 440 445
 Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His
 450 455 460
 Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr
 465 470 475 480
 Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val
 485 490 495
 Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu
 500 505 510
 Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr
 515 520 525
 Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly
 530 535 540
 Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
 545 550 555 560
 Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
 565 570 575
 Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
 580 585 590
 Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
 595 600 605
 Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
 610 615 620
 Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
 625 630 635 640
 Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
 645 650 655
 Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
 660 665 670
 Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
 675 680 685
 Val Pro Ala Ala
 690

<210> 20
 <211> 1464
 <212> DNA
 <213> Unknown

<220>
 <223> Nucleotide sequence of K:trAPAO translational

fusion with barley alpha amylase signal sequence,
 for expression and secretion of the mature trAPAO
 in maize. Nucleotides 1-72, barley alpha amylase
 signal sequence, nucleotides 73-75, added lysine
 residue; nucleotides 76 -1464 , trAPAO cDNA.

```

<221> sig_peptide
<222> (1)...(72)
<223> Barley alpha amylase signal sequence

<221> misc_feature
<222> (73)...(1464)
<223> K:trAPAOcDNA

<221> CDS
<222> (1)...(1461)

<221> misc_feature
<222> (73)...(75)
<223> Added lysine residue

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Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
          -20           -15           -10

ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta      96
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val
          -5            1            5

gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag      144
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
          10           15           20

gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg      192
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
          25           30           35           40

gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac      240
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
          45           50           55

gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc      288
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
          60           65           70

aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act      336
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
          75           80           85

gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct      384
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro
          90           95           100

tat ggt gag tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa      432
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
          105          110          115          120

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ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp 125 130 135	480
ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala 140 145 150	528
cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala 155 160 165	576
aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser 170 175 180	624
atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn 185 190 195 200	672
att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr 205 210 215	720
ggg atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly 220 225 230	768
tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser 235 240 245	816
ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys 250 255 260	864
gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser 265 270 275 280	912
cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu 285 290 295	960
ggc tac tat agc aag ata gtc ttc gta tgg gac aag cgg tgg tgg cgc Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg 300 305 310	1008
gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser 315 320 325	1056
ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr 330 335 340	1104
tgt ttc atg gtc gga gac ccg gga egg aag tgg tcc caa cag tcc aag 25	1152

Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys			
345	350	355	360
cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag			1200
Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu			
365	370	375	
aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag			1248
Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu			
380	385	390	
tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg			1296
Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly			
395	400	405	
ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag			1344
Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys			
410	415	420	
agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat			1392
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr			
425	430	435	440
atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg			1440
Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val			
445	450	455	
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<211> 487
<212> PRT
<213> Unknown

<220>
<221> SIGNAL
<222> (1)...(24)

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Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln			
10	15	20	
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly			
25	30	35	40
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn			
45	50	55	
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser			
60	65	70	
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr			
75	80	85	
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro			
26			

90	95	100													
Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu
105						110				115					120
Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	Asp
						125			130						135
Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala
						140			145						150
His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala
						155			160						165
Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser
						170			175						180
Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn
						185			190						200
Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr
						205			210						215
Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly
						220			225						230
Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser
						235			240						245
Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys
						250			255						260
Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser
						265			270						280
Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu
						285			290						295
Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg
						300			305						310
Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser
						315			320						325
Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr
						330			335						340
Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys
						345			350						360
Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu
						365			370						375
Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu
						380			385						390
Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly
						395			400						405
Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys
						410			415						420
Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr
						425			430						440
Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val
						445			450						455
Ala	Ser	Leu	Val	Pro	Ala	Ala									
						460									

<210> 22

<211> 1803

<212> DNA

<213> Exophiala spinifera

<220>

<221> CDS

<222> (1)...(1800)

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gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	30	96
20 25 30		
aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	45	144
35 40 45		
gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	60	192
50 55 60		
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	80	240
65 70 75 80		
tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	95	288
85 90 95		
ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	110	336
100 105 110		
cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	125	384
115 120 125		
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg Thr Ala Leu Val Pro Gly His Thr Pro Asp Asn Val Ala Asp Val	140	432
130 135 140		
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val	160	480
145 150 155 160		
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val	175	528
165 170 175		
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile	190	576
180 185 190		
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val	205	624
195 200 205		
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr	220	672
210 215 220		
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala	28	720

225	230	235	240	
cct tat gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 245		250		768
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 260		265		816
gac ctc aag gcg agc cct cag gcg aag cg ^g ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 275		280		864
g ^c g cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 290		295		912
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 305		310		960
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 325		330		1008
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 340		345		1056
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 355		360		1104
g ^c c tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 370		375		1152
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 385		390		1200
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 405		410		1248
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 420		425		1296
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp 435		440		1344
cg ^c gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile 450		455		1392
		460		

115	120	125
Thr Ala Leu Val Pro Gly His	Thr Thr Pro Asp Asn Val	Ala Asp Val
130	135	140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val		
145	150	155
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val		
165	170	175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile		
180	185	190
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val		
195	200	205
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr		
210	215	220
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala		
225	230	235
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala		
245	250	255
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln		
260	265	270
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe		
275	280	285
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val		
290	295	300
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile		
305	310	315
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser		
325	330	335
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys		
340	345	350
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro		
355	360	365
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala		
370	375	380
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys		
385	390	395
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe		
405	410	415
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile		
420	425	430
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp		
435	440	445
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile		
450	455	460
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile		
465	470	475
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser		
485	490	495
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr		
500	505	510
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile		
515	520	525
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr		
530	535	540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe		
545	550	555
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly		
565	570	575
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val		

580	585	590
Val Ala Ser Leu Val Pro Ala Ala		
595	600	
<210> 24		
<211> 3003		
<212> DNA		
<213> Unknown		
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<223> Sequence is barley alpha amylase signal sequence:		
espl mat: an artificial spacer sequence and		
K:trAPAO		
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<233> Barley alpha amylase signal sequence		
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<231> misc_feature		
<232> (1612)...(3000)		
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<232> (1612)...(1614)		
<233> Extra lysine		
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Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly		
-20	-15	-10
ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct		96
Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala		
-5	1	5
ggg atg gtg gtc ggc acg act act act gtc ccc ggc acc act gcg acc		144
Gly Met Val Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr		
10	15	20
gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt		192
Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe		
25	30	35
40		
gct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act		240
Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr		
45	50	55
55		
32		

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cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly	336
75 80 85	
gaa aat gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu	384
90 95 100	
aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Ala Leu Glu	432
105 110 115 120	
tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala	480
125 130 135	
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu	528
140 145 150	
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly	576
155 160 165	
ttc cta gac caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala	624
170 175 180	
gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala	672
185 190 195 200	
ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro	720
205 210 215	
ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe	768
220 225 230	
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu	816
235 240 245	
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp	864
250 255 260	
ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu	912
265 270 275 280	
tac acg ttg gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc	960

Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg			
285	290	295	
acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc			1008
Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala			
300	305	310	
aac gac gga ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat			1056
Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr			
315	320	325	
ctc gag gag gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt			1104
Leu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu			
330	335	340	
gga gca tat ccc att gga tcc cca ggg atc gga tcg cct caa gat cag			1152
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln			
345	350	355	360
att gcc gcc att gag acc gag gta aga ttc cag tgt cct tct gcc atc			1200
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile			
365	370	375	
gtg gct cag gac tcc cg ^g aat cgg ggt atc cct tct tgg cgc tac tac			1248
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr			
380	385	390	
tac aat gcg acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg			1296
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val			
395	400	405	
tac cac agc tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca			1344
Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala			
410	415	420	
agt gcg acc gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc			1392
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala			
425	430	435	440
tgg gcg gcc ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa			1440
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln			
445	450	455	
gtg ccg aat gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt			1488
Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val			
460	465	470	
gac gtc tct cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt			1536
Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg			
475	480	485	
tat tat act gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc			1584
Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly			
490	495	500	
agc ggc gga ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg			1632
Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val			
505	510	515	520

gta gtg gtc ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val 525 530 535	1680
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val 540 545 550	1728
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile 555 560 565	1776
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 570 575 580	1824
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 585 590 595 600	1872
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala 605 610 615	1920
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 620 625 630	1968
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 635 640 645	2016
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 650 655 660	2064
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 665 670 675 680	2112
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 685 690 695	2160
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 700 705 710	2208
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 715 720 725	2256
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 730 735 740	2304
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca	2352

Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala			
745	750	755	760
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa			2400
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys			
765	770	775	
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt			2448
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe			
780	785	790	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc			2496
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile			
795	800	805	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccc tgg tgg			2544
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp			
810	815	820	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc			2592
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile			
825	830	835	840
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att			2640
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile			
845	850	855	
acc tgt ttc atg gtc gga gac ccg gga cggt aag tgg tcc caa cag tcc			2688
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser			
860	865	870	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac			2736
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr			
875	880	885	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc			2784
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile			
890	895	900	
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat			2832
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr			
905	910	915	920
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc			2880
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe			
925	930	935	
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg			2928
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly			
940	945	950	
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt			2976
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val			
955	960	965	
gtg gct agc ctg gtg cca gca gca tag			3003
Val Ala Ser Leu Val Pro Ala Ala			

970

975

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 <212> PRT
 <213> Unknown

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 -5 1 5
 Gly Met Val Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
 10 15 20
 Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
 25 30 35 40
 Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr
 45 50 55
 Ala 'Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu
 60 65 70
 Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Ser Ala Gly
 75 80 85
 Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu
 90 95 100
 Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu
 105 110 115 120
 Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala
 125 130 135
 Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu
 140 145 150
 Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly
 155 160 165
 Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala
 170 175 180
 Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala
 185 190 195 200
 Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro
 205 210 215
 Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe
 220 225 230
 Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu
 235 240 245
 Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp
 250 255 260
 Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu
 265 270 275 280
 Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg
 285 290 295
 Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala
 300 305 310
 Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr
 315 320 325
 Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu

330	335	340
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln		
345	350	355
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile		360
365	370	375
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr		
380	385	390
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val		
395	400	405
Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala		
410	415	420
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala		
425	430	435
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln		440
445	450	455
Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val		
460	465	470
Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg		
475	480	485
Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly		
490	495	500
Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val		
505	510	515
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val		
525	530	535
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val		
540	545	550
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile		
555	560	565
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val		
570	575	580
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr		
585	590	595
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala		
605	610	615
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala		
620	625	630
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln		
635	640	645
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe		
650	655	660
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val		
665	670	675
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile		
685	690	695
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser		
700	705	710
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys		
715	720	725
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro		
730	735	740
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala		
745	750	755
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys		
765	770	775
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe		
780	785	790
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile		

795	800	805
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp		
810	815	820
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile		
825	830	835
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile		
845	850	855
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser		
860	865	870
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr		
875	880	885
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile		
890	895	900
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr		
905	910	915
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe		
925	930	935
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly		
940	945	950
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val		
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Val Ala Ser Leu Val Pro Ala Ala		
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<223> Barley alpha amylase signal sequence: BEST1
mature: artificial spacer: and K:trAPAO. For
plant expression.

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<233> Barley alpha amylase signal sequence

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<321> misc_feature

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205	210	215	
cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg		768	
Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser			
220	225	230	
ggc gag cgc ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca		816	
Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro			
235	240	245	
gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccc gca tcg cgg gac		864	
Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp			
250	255	260	
ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg		912	
Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu			
265	270	275	280
ccg cag acc gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccc gtt		960	
Pro Gln Thr Asp Ser Ala Ala Ile Ala Gly Gln Leu Ala Pro Val			
285	290	295	
cgg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg		1008	
Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly			
300	305	310	
cgc ggg ccc atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg		1056	
Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala			
315	320	325	
cag ttt ggc gac caa gcc gcc gtc gtg gcg gcg tgc tat ccc ctc gac		1104	
Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp			
330	335	340	
ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat		1152	
Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn			
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cag ttc aat cgg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag		1200	
Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln			
365	370	375	
ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga		1248	
Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly			
380	385	390	
aga gcg ccc gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg		1296	
Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val			
395	400	405	
ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccc gag ggg ccc		1344	
Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro			
410	415	420	
acg ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc		1392	
Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val			

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Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala	Leu Thr Trp Pro			
445	450	455		
gcttatctacggcagaatcgaccatgtaca	ttcggttcccggcgccgc			1488
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe	Gly Pro Glu Gly Arg			
460	465	470		
gcggcggtgtgtcgccccggaccttccatccccttgcgcgat	ggc			1536
Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro	Pro Cys Ala Asp Gly			
475	480	485		
gcgaaggcgggggcggcggcagcggcggcggcggcggcggc	ggc			1584
Ala Lys Ala Gly Gly Ser Gly Gly Ser Gly Gly	Ser Gly Gly Ser			
490	495	500		
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc	gct ggc ttg agc ggt			1632
Lys Asp Asn Val Ala Asp Val Val Val Gly	Ala Gly Leu Ser Gly			
505	510	515	520	
tttgagacgca cgc aaa gtc cag gcc ggc ggt ctg	tcc tgc ctc gtt			1680
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly	Leu Ser Cys Leu Val			
525	530	535		
ctt gag gcg atg gat cgt gta ggg gga aag act	ctg agc gta caa tcg			1728
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr	Leu Ser Val Gln Ser			
540	545	550		
ggtcgcaggaggactatcAACGACTCTGGCCTGTTGGATCAAT	AAT			1776
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly	Ala Trp Ile Asn			
555	560	565		
gac agc aac caa agc gaa gta tcc aga ttg ttt	gaa aga ttt cat ttg			1824
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe	Glu Arg Phe His Leu			
570	575	580		
gagggcggagctc cagaggacgactggaaat tcaatc	cat caa gca caa			1872
Glu Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile	His Gln Ala Gln			
585	590	595	600	
gac ggt acaccactaca gct cct tat ggt gac tcc	ttgtcgtcagcgg			1920
Asp Gly Thr Thr Ala Pro Tyr Gly Asp Ser Leu	Leu Ser Glu			
605	610	615		
gaggttgcagtgcacccgttgcggaa ctc ctc ccc	gtatggttctcagctg			1968
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro	Val Trp Ser Gln Leu			
620	625	630		
atc gaa gag cat agc ctt caa gac ctc aag	gcg agc ctc cag gcg aag			2016
Ile Glu His Ser Leu Gln Asp Leu Lys Ala Ser	Pro Gln Ala Lys			
635	640	645		
cggctc gac agt gtg agc ttc	gac cac tac tgt gag aag gaa cta aac			2064
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys	Glu Lys Glu Leu Asn			
650	655	660		

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Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu		
665 670 675 680		
ggg gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc		3160
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile		
685 690 695		
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc		3208
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Asp Gly		
700 705 710		
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc		3256
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala		
715 720 725		
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc		3304
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val		
730 735 740		
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg		3352
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser		
745 750 755 760		
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Gly Ala Val Phe Arg Ser Lys Val Val Val Ser Leu Pro Thr Thr		
765 770 775		
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Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln		
780 785 790		
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc		3496
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe		
795 800 805		
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc		3544
Val Trp Asp Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu		
810 815 820		
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac		3592
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp		
825 830 835 840		
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga		3640
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly		
845 850 855		
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg		3688
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp		
860 865 870		
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag		3736
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu		
875 880 885		
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa		3784
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln		

890	895	900	
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905	910	915	920
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			2880
925	930	935	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			2928
940	945	950	
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<p>Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn 125 130 135</p>			
<p>Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr 140 145 150</p>			
<p>Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg 155 160 165</p>			
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 205 210 215
 Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser
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 Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro
 235 240 245
 Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp
 250 255 260
 Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu
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 Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val
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 Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly
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 Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala
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 Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp
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 Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn
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 Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly
 380 385 390
 Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val
 395 400 405
 Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro
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 Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val
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 Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro
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 Ala Tyr Ser Thr Gly Lys Ser 'Thr Met Thr Phe Gly Pro Glu Gly Arg
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 475 480 485
 Ala Lys Ala Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
 490 495 500
 Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly
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 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 525 530 535
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
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 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
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 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
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 Glu Val Ala Ser Ala Leu Ala Glu Leu Ile Pro Val Trp Ser Gln Leu
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 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
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 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 650 655 660

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
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 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
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 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
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 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
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 765 770 775
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 780 785 790
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 795 800 805
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
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 Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
 825 830 835 840
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 845 850 855
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 860 865 870
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 875 880 885
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 890 895 900
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<212> DNA

<213> Unknown

<220>

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2227-3615, K:trAPAO, 3616-3618, stop codon. For
bacterial expression.

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1				5					10					15			

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 Thr Arg Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45

ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
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gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt
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 100 105 110

aaa gar ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125

atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140

ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160

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Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu			
165	170	175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac			576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr			
180	185	190	
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Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala			
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Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg			
210	215	220	
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Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val			
225	230	235	240
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Val Gly Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu			
245	250	255	
ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt gcg cct cct			816
Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro			
260	265	270	
act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act gca tat ggt			864
Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly			
275	280	285	
cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc cgt gag att			912
Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile			
290	295	300	
acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt gaa agt gag			960
Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu			
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gac tgc ctg aac ctc aac atc tac gtc cca gga act gag aac aca aac			1008
Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn			
325	330	335	
aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa tat ggt tgg			1056
Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp			
340	345	350	
aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc aat cag gat			1104
Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp			
355	360	365	
gtc atc gcc gtg acc atc aac tac aga acg aac att ctg ggg ttc cct			1152
Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro			
370	375	380	
gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg ttc cta gac			1200
Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp			
385	390	395	400

caa agg ttt gct ttg gat tgg gta cag cg ^g aac atc gca gcc ttt ggc Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly	1248
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420 425 430	
agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca ccc ttc cga Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg	1344
435 440 445	
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450 455 460	
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465 470 475 480	
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485 490 495	
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500 505 510	
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515 520 525	
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530 535 540	
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545 550 555 560	
gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt gga gca tat Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr	1728
565 570 575	
ccc att gga tcc cca ggg atc gga tcg cct caa gat cag att gcc gcc Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala	1776
580 585 590	
att gag acc gag gta aga ttc cag tgt cct tct gcc atc gtg gct cag Ile Glu Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln	1824
595 600 605	
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610 615 620	
acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg tac cac agc	1920

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Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr			
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gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc tgg gcg gcc			2016
Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala			
660	665	670	
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Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn			
675	680	685	
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Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser			
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Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr			
705	710	715	720
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Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Ser Gly Gly			
725	730	735	
ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg gta gtg gtg			2256
Gly Ser Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val			
740	745	750	
ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc			2304
Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala			
755	760	765	
ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag			2352
Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys			
770	775	780	
act ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc			2400
Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu			
785	790	795	800
ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg			2448
Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu			
805	810	815	
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Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn			
820	825	830	
tca atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt			2544
Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly			
835	840	845	
gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc			2592
Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu			
850	855	860	

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cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys 980 985 990	2976
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Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala			
1105	1110	1115	1120
ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg			3408
Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser			
1125	1130	1135	
aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac			3456
Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn			
1140	1145	1150	
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Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val			
1155	1160	1165	
cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa			3552
His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu			
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Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser			
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Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu			
35 40 45			
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys			
50 55 60			
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn			
65 70 75 80			
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu			
85 90 95			
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser			
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Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu			
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Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn			
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Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp			
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 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
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 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
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 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
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 Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val
 225 230 235 240
 Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu
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 Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro
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 Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly
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 Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile
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 Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu
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 Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn
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 Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp
 340 345 350
 Asn Ser Phe His Leu 'Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp
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 Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro
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 Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp
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 Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly
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 Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg
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 Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg
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 Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly
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 Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr
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 Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr
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 Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg Thr Thr Gly
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 Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly
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 Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala
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 Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala
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 Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr
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 Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr Gly
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 Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr
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 Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val
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 His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys
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 Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val
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 1155 1160 1165
 His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu
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 Leu Val Pro Ala Ala
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 bacterial expression vector pGEX-4T-1 or similar
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 + polylinker, 688-2163, BEST1 mature; 2164-2199,
 spacer, 2200-3588, K:trAPAO

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10

15

55

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
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tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggt ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
ggt gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt	672
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
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gga tcc ccg gaa ttc acg gat ttt ccg gtc cgc agg acc gat ctg ggc	720
Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly	
225 230 235 240	
cag gtt cag gga ctg gcc ggg gac gtg atg age ttt cgc gga ata ccc	768

Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro			
245	250	255	
tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg ccc caa cac			816
Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His			
260	265	270	
gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt ggc tcc gac			864
Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp			
275	280	285	
tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc ccc ggc gtg			912
Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val			
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agc gag gac tgt ctt tac ctc aac gta tgg gcg cgc tca ggc gct aaa			960
Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys			
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ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc ggc ttc gcc			1008
Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Phe Ala			
325	330	335	
ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg ctt gcg cga			1056
Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg			
340	345	350	
cag ggc gtc gtc gtg acg ttt aac tat cgg acg aac atc ctc ggc			1104
Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly			
355	360	365	
ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc gga act tcg			1152
Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser			
370	375	380	
ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg tgg gtg cag			1200
Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln			
385	390	395	400
agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg acg gtc ttt			1248
Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe			
405	410	415	
ggt gaa tcg gcc gga ggg agc gcg atc gga ctt ctg ctc acc tcg ccc			1296
Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro			
420	425	430	
ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt cca ggg ctg			1344
Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu			
435	440	445	
acg cga ccg ctc gcg acg ctc gcc gac agc gcc ggc tcg ggc gag cgc			1392
Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg			
450	455	460	
ctc gac gcc gat ctt tgg cga ctg cgc tcg acc gac cca gcc acc ctg			1440
Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu			
465	470	475	480

atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac ctg cgc agg		1488
Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg		
485	490	495
ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg ccg cag acc		1536
Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr		
500	505	510
gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt cgg gtc ctg		1584
Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu		
515	520	525
atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg cgc gcg ccg		1632
Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly Arg Ala Pro		
530	535	540
atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg cag ttt ggc		1680
Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala Gln Phe Gly		
545	550	555
560		
gac caa gcc gcc gtc gcg gcg tgc tat ccc ctc gac ggc cgg gcc		1728
Asp Gln Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp Gly Arg Ala		
565	570	575
acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat cag ttc aat		1776
Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn		
580	585	590
ccg ggg gtc tcg gcc ttc tcg gaa gcg ctt gtg cgc cag ggc gcg ccc		1824
Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln Gly Ala Pro		
595	600	605
gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga aga gcg ccc		1872
Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Arg Ala Pro		
610	615	620
gct acc cac gga gaa att ccc tac gtt ttc ggg gtg ttc aag ctc		1920
Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu		
625	630	635
640		
gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc acg ccc gcc		1968
Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala		
645	650	655
gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc cgg ttc gcc		2016
Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala		
660	665	670
aag aat ggc gac ccc ggg gac gcc ctt acc tgg cct gcc tat tct		2064
Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro Ala Tyr Ser		
675	680	685
acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc gcg gtc		2112
Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val		
690	695	700
gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc gcc aag gcg		2160

Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala			
705	710	715	720
ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc aaa gac aac			2208
Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn			
725	730	735	
gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg			2256
Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr			
740	745	750	
gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag geg			2304
Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala			
755	760	765	
atg gat cgt gta ggg gga aag act ctg agc gta caa tcg ggt ccc ggc			2352
Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly			
770	775	780	
agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac			2400
Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn			
785	790	795	800
caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag			2448
Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu			
805	810	815	
ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt aca			2496
Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr			
820	825	830	
acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca			2544
Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala			
835	840	845	
agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag			2592
Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu			
850	855	860	
cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac			2640
His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp			
865	870	875	880
agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct			2688
Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala			
885	890	895	
gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa			2736
Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu			
900	905	910	
gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc			2784
Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala			
915	920	925	
acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat			2832
Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr			
930	935	940	

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gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp 1025 1030 1035 1040	3120
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35 40 45
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
50 55 60
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
65 70 75 80
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
85 90 95
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
100 105 110
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
115 120 125
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
130 135 140
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
145 150 155 160
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
165 170 175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
180 185 190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
195 200 205
Thr Phe Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
210 215 220
Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly
225 230 235 240
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245 250 255
Tyr Ala Ala Pro Pro Val Gly Leu Arg Trp Lys Pro Pro Gln His
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Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp
275 280 285
Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val
290 295 300
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305 310 315 320
Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala
325 330 335
Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg
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Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly
 355 360 365
 Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser
 370 375 380
 Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln
 385 390 395 400
 Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe
 405 410 415
 Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro
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 Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu
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 Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg
 450 455 460
 Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu
 465 470 475 480
 Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg
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 Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr
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 Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu
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 Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp Gly Arg Ala
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 Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn
 580 585 590
 Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln Gly Ala Pro
 595 600 605
 Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly Arg Ala Pro
 610 615 620
 Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu
 625 630 635 640
 Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala
 645 650 655
 Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala
 660 665 670
 Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro Ala Tyr Ser
 675 680 685
 Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val
 690 695 700
 Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala
 705 710 715 720
 Gly Gly Gly Ser Gly Gly Ser Gly Gly Ser Lys Asp Asn
 725 730 735
 Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr
 740 745 750
 Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala
 755 760 765
 Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly
 770 775 780
 Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn
 785 790 795 800
 Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu
 805 810 815
 62

Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr
 820 825 830
 Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala
 835 840 845
 Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu
 850 855 860
 His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp
 865 870 875 880
 Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala
 885 890 895
 Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu
 900 905 910
 Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala
 915 920 925
 Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr
 930 935 940
 Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys
 945 950 955 960
 Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile
 965 970 975
 Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val
 980 985 990
 Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro
 995 1000 1005
 Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala
 1010 1015 1020
 Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp
 1025 1030 1035 1040
 Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser
 1045 1050 1055
 Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg
 1060 1065 1070
 Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp
 1075 1080 1085
 Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu
 1090 1095 1100
 Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn
 1105 1110 1115 1120
 Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro
 1125 1130 1135
 Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu
 1140 1145 1150
 Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu
 1155 1160 1165
 Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly
 1170 1175 1180
 Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 1185 1190 1195

<210> 32
 <211> 1803
 <212> DNA
 <213> Unknown

 <220>
 <231> CDS
 <232> (1)...(1803)

<223> Glyc(-)APAO coding sequence; mutation in putative glycosylation sites

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Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
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gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg 96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Arg Tyr Val
20 25 30

aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct 144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
35 40 45

gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc 192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60

ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac 240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80

tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg 288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95

ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg 336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110

cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc 384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg 432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
130 135 140

gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc 480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160

cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta 528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175

ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc 576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
180 185 190

aac gac ctc ggc gct gcg tgg atc aat gat agc aat cag gcc gaa gta 624
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val
195 200 205

tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg 672
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr

210	215	220	
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala	225	230	720
235		240	
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala	245	250	768
255			
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln	260	265	816
270			
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe	275	280	864
285			
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val	290	295	912
300			
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile	305	310	960
315		320	
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser	325	330	1008
335			
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys	340	345	1056
350			
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro	355	360	1104
365			
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala	370	375	1152
380			
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys	385	390	1200
395		400	
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe	405	410	1248
415			
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile	420	425	1296
430			
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	435	440	1344
445			

cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc		1392	
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile			
450	455	460	
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att		1440	
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile			
465	470	475	480
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc		1488	
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser			
485	490	495	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac		1536	
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr			
500	505	510	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc		1584	
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile			
515	520	525	
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat		1632	
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr			
530	535	540	
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc		1680	
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe			
545	550	555	560
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg		1728	
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly			
565	570	575	
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt		1776	
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val			
580	585	590	
gtg gct agc ctg gtg cca gca gca tag		1803	
Val Ala Ser Leu Val Pro Ala Ala *			
595	600		

<210> 33
 <211> 600
 <212> PRT
 <213> Unknown

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 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
 35 40 45
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
 65 70 75 80
 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
 66

85	90	95
Leu Lys Ala Thr Phe Ala Leu Asp Arg	Leu Pro Pro Cys	Thr Leu Val
100	105	110
Pro Val Ser Ala Leu Ser Ser Pro	Glu Tyr Leu Phe Glu Val Asp Ala	
115	120	125
Thr Ala Leu Val Pro Gly His	Thr Thr Pro Asp Asn Val Ala Asp Val	
130	135	140
Val Val Val Gly Ala Gly Leu Ser Gly	Leu Glu Thr Ala Arg Lys Val	
145	150	155
Gln Ala Ala Gly Leu Ser Cys	Leu Val Leu Glu Ala Met Asp Arg Val	
165	170	175
Gly Gly Lys Thr Leu Ser Val Gln Ser	Gly Pro Gly Arg Thr Thr Ile	
180	185	190
Asn Asp Leu Gly Ala Ala Trp	Ile Asn Asp Ser Asn Gln Ala Glu Val	
195	200	205
Ser Arg Leu Phe Glu Arg Phe His	Leu Glu Gly Glu Leu Gln Arg Thr	
210	215	220
Thr Gly Asn Ser Ile His	Gln Ala Gln Asp Gly Thr Thr Thr Ala	
225	230	235
Pro Tyr Gly Asp Ser Leu Leu Ser	Glu Val Ala Ser Ala Leu Ala	
245	250	255
Glu Leu Leu Pro Val Trp Ser Gln	Leu Ile Glu Glu His Ser Leu Gln	
260	265	270
Asp Leu Lys Ala Ser Pro Gln	Ala Lys Arg Leu Asp Ser Val Ser Phe	
275	280	285
Ala His Tyr Cys Glu Lys Glu	Leu Asn Leu Pro Ala Val Leu Gly Val	
290	295	300
Ala Asn Gln Ile Thr Arg	Ala Leu Leu Gly Val Glu Ala His Glu Ile	
305	310	315
Ser Met Leu Phe Leu Thr Asp Tyr	Ile Lys Ser Ala Thr Gly Leu Ser	
325	330	335
Asn Ile Phe Ser Asp Lys Lys Asp	Gly Gln Tyr Met Arg Cys Lys	
340	345	350
Thr Gly Met Gln Ser Ile Cys His	Ala Met Ser Lys Glu Leu Val Pro	
355	360	365
Gly Ser Val His Leu Asn Thr	Pro Val Ala Glu Ile Glu Gln Ser Ala	
370	375	380
Ser Gly Cys Thr Val Arg Ser	Ala Ser Gly Ala Val Phe Arg Ser Lys	
385	390	395
Lys Val Val Val Ser Leu Pro Thr	Thr Leu Tyr Pro Thr Leu Thr Phe	
405	410	415
Ser Pro Pro Leu Pro Ala Glu Lys	Gln Ala Leu Ala Glu Asn Ser Ile	
420	425	430
Leu Gly Tyr Tyr Ser Lys Ile Val	Phe Val Trp Asp Lys Pro Trp Trp	
435	440	445
Arg Glu Gln Gly Phe Ser Gly Val	Leu Gln Ser Ser Cys Asp Pro Ile	
450	455	460
Ser Phe Ala Arg Asp Thr	Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	
465	470	475
Thr Cys Phe Met Val Gly Asp Pro	Gly Arg Lys Trp Ser Gln Gln Ser	
485	490	495
Lys Gln Val Arg Gln Lys Ser Val	Trp Asp Gln Leu Arg Ala Ala Tyr	
500	505	510
Glu Asn Ala Gly Ala Gln Val	Pro Glu Pro Ala Asn Val Leu Glu Ile	
515	520	525
Glu Trp Ser Lys Gln Gln Tyr	Phe Gln Gly Ala Pro Ser Ala Val Tyr	
530	535	540
Gly Leu Asn Asp Leu Ile Thr	Leu Gly Ser Ala Leu Arg Thr Pro Phe	

545	550	555	560												
Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly
565								570						575	
Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val
580								585						590	
Val	Ala	Ser	Leu	Val	Pro	Ala	Ala								
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<220> <223> 37-mer oligonucleotide															
<400> 34 ggggaattca tggcacttgc accgagctac atcaatc															
37															
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<221> intron <222> (1134)...(1186)															
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120															
gacgctttgg gcgtgacaga cccagctac gagaaacagg ttgccccagg attcgccaaat															
180															
ctgcgagctt gccttgcgtc agttggagcc tcttcaaagc acgtcaccaa gctcaattac															
240															
tacatcgctg actacgcccc gagcaaactc accgcaattt gagatggct gaagtctacc															
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gaataacctt ttgaggttga tgccacggcg ctggtgccag gacactcgac cccagacaaac															
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aatgacagca accaaagcga agtatecaga ttgtttgaaa gatttcattt ggagggcgag															
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agaatacagt cactgactcc acttgcgtcca gctgagcgag gaggttgcaa gtgcacttgc															
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1020															
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taatattgtc tcggacaaga aagacggcg ggactatatg cgtatcaaaa caggttgttg															
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cggtgtccctc tcaggttaggg gactcggttc ttgtgttca ttccaggat gcaatcgat															
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1560															

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gtacgacaaa	agtctgtctg	ggaccaactc	cgcgcagcct	acgagaacgc	cggggcccaa	1680
gtccccagagc	cggccaacgt	gctcgaaatc	gagtggtcga	agcagcagta	tttccaagg	1740
gctccgagcg	cctgttatgg	gctgaacgt	ctcatcacac	tgggtcggc	gctcagaacg	1800
ccgttcaagt	gtgttcattt	cgttggAACG	gagacgtctt	tagttggaa	agggtatatg	1860
gaaggggcca	tacgatcggg	tcaacgaggt	gctgcagaag	ttgtggctag	cctggtgcca	1920
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 <212> PRT
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 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Leu Gly Val Thr Asp Pro
 35 40 45
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60
 Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr
 65 70 75 80
 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
 85 90 95
 Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
 100 105 110
 Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
 115 120 125
 Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
 130 135 140
 Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
 145 150 155 160
 Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
 165 170 175
 Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
 180 185 190
 Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
 195 200 205
 Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
 210 215 220
 Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
 225 230 235 240
 Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
 245 250 255
 Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu
 260 265 270
 Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
 275 280 285
 Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val
 290 295 300
 Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
 305 310 315 320
 Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
 325 330 335
 Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
 340 345 350

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
 355 360 365
 Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala
 370 375 380
 Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
 385 390 395 400
 Lys Val Val Val Ser Leu Pro Thr Leu Tyr Pro Thr Leu Thr Phe
 405 410 415
 Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile
 420 425 430
 Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp
 435 440 445
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
 450 455 460
 Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile
 465 470 475 480
 Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
 485 490 495
 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
 500 505 510
 Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
 515 520 525
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
 530 535 540 560
 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
 545 550 555 575
 Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
 565 570 575
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
 580 585 590
 val Ala Ser Leu Val Pro Ala Ala
 595 600

<210> 37

<211> 1929

<212> DNA

<213> Exophiala spinifera

<220>

<221> intron

<222> (739)...(811)

<221> intron

<222> (1134)...(1186)

<400> 37

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gacgctttgg gcgtgacaga cccagcctac gagaacacagg ttgcccaagg attcgccaat	180
ctgcgagctt gccttgctgc agttggagcc tcttcaaacc acgtccaaac gctcaattac	240
tacatcgtcg actacgcccc gagcaaactc accgcaattt gatatgggct gaagtctacc	300
tttgccttg acaggctccc tccttgcacg ctggtgccag taccggcctt ggcttcacct	360
gaataacctt ttgaggttga cgccacggcg ctggtgccag gacactcgac cccagacaac	420
gttgcggacg ttgtagttgg gggcgctggc tttagcgatgg atcgtgttagg gggaaagact	480
caggccgccc gtctgttctg cctcggttctt gaggcgatgg acctcggcgc tgcgtggatc	540
ctgagcgtac aatcggttcc cggcaggacg actatcaacg acctcggcgc tgcgtggatc	600
aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcatt ggagggcgag	660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtaaac cactacagct	720

ccttatggtg	actccccgt	aagcacaatc	ccactttgtg	atgagacctc	tgtcgagtgt	780
agaatacagt	cactgactcc	acttcgtcca	getgagcga	gagggtgcaa	gtgcacttgc	840
ggaactcctc	cccgtatggt	ctcagctgat	cgaagagtat	agccttgaag	accccaaggc	900
gagccctcag	gCGAAGCggc	tcgacagtgt	gagcttcg	cactactgtg	agaaggac	960
aaacttgcct	gctgttctca	gcgtggcaaa	ccagatcaca	cgcgcctgc	tcggtgtgga	1020
agccccacgag	atcagcatgc	tttttctcac	cgactacatc	aagagtgcc	ccggctctcag	1080
taatattgtc	tcggacaaga	aagacggcgg	gca	gatgtat	cgatgaaaaa	1140
cggtgtcctc	tcaggttaggg	gactcg	tttagtggta	ttccaggat	gcagtcgatt	1200
tgccatgcca	tgtcaaagga	acttgc	ttccatgc	accta	acac cccgtcgt	1260
ggaatttgagc	agtcggcg	cggtgtata	gtacgatcg	cctcggcgc	cgtgttccga	1320
agcaaaaagg	tgggtgtt	tttaccgaca	acattgtatc	ccac	tttgcacca	1380
cctcttccc	ccgagaagca	agcattggcg	gaaaaatcta	tcctcg	ctatagcaag	1440
atagtctcg	tatggacaa	cccgtgg	cgcgaaca	gcttc	tcggc	1500
tcgagctgt	acccatc	at	tcgaa	tcgaa	tcggcaat	1560
tccattac	tttcatgtt	cgagaccc	ggacggaa	ggtcc	aca	1620
gtacgacaaa	agtctgt	ggaccaactc	cgcgc	acgagaac	cgccccaa	1680
gtcccagagc	cgccaa	gtcgaa	gagtgg	agcagc	tttcaagga	1740
gctccgagc	ccgtctatgg	gctga	acat	tc	tcggc	1800
ccgttcaagt	gtgttcattt	cg	tttggaa	agg	gtat	1860
gaaggggcca	tacgatcggg	tcaac	gaggt	gtc	gaga	1920
gcagcatag						1929

<210> 38

<211> 600

<212> PRT

<213> Exophiala spinifera

<400> 38

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro
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Ala	Gly	Tyr	Ser	His	Ile	Gly	Val	Gly	Pro	Asn	Glu	Ala	Arg	Tyr	Val
					20			25				30			
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Leu	Gly	Val	Thr	Asp	Pro
					35			40				45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
					50			55				60			
Leu	Ala	Ala	Val	Gly	Ala	Ser	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
					65			70			75				80
Tyr	Ile	Val	Asp	Tyr	Ala	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
					85			90				95			
Leu	Lys	Ser	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
					100			105				110			
Pro	Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala
					115			120				125			
Thr	Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
					130			135				140			
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
					145			150			155				160
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
					165			170				175			
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile
					180			185				190			
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
					195			200				205			
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr
					210			215				220			
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala
					225			230			235				240

Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
 245 250 255
 Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu
 260 265 270
 Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
 275 280 285
 Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val
 290 295 300
 Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
 305 310 315 320
 Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
 325 330 335
 Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
 340 345 350
 Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
 355 360 365
 Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala
 370 375 380
 Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
 385 390 395 400
 Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
 405 410 415
 Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile
 420 425 430
 Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp
 435 440 445
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
 450 455 460
 Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile
 465 470 475 480
 Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
 485 490 495
 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
 500 505 510
 Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
 515 520 525
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
 530 535 540
 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
 545 550 555 560
 Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
 565 570 575
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
 580 585 590
 Val Ala Ser Leu Val Pro Ala Ala
 595 600

<210> 39
 <211> 1930
 <212> DNA
 <213> Exophiala spinifera

<220>
 <221> intron
 <222> (739) ... (811)

<221> intron
 <222> (1134) ... (1187)

<221> misc_feature
 <222> (648)...(648)
 <223> n = A,T,C or G

<400> 39

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cacgtcgccg taggcccaga cggagggagg tatgtacaa tagctggaca	gattggacaa	120
gacgcgtcg gcggtacaga ccctgcctac gagaaaacagg ttgccaagc	attcgccaat	180
ctgcgagctt gccttgctgc agttggagcc acttcaaagc acgtcaccaa	gctcaattac	240
tacatcgctg actacgcccc gagcaaactc acgcattg gagatggct	gaaggctacc	300
tttgccttg acaggctccc tccttgcacg ctgggtgccag tgcgcctt	gtcttcacct	360
gaataacctt ttgaggttga tgccacggcg ctgggtgccgg gacacacgac	cccagacaac	420
gttgcggacg tggtagtggt gggcgctggc ttgagcggtt tggagacggc	acgcaaagtc	480
caggcccgccg gtctgtcctg cctcgtttt gaggegatgg atcgtgttagg	gggaaagact	540
ctgagcgtaa aatcggtcc cggcaggacg actatcaacg acctcggcgc	tgcgtggatc	600
aatgacacga accaaagcga agtacccaga ttgtttgaaa gatttcatnt	ggagggcggag	660
ctccagagga cgactggaaa ttcaatccat caagcacaag acggtacaac	cactacagct	720
ccttatggtg actccttggt aagcacaatc ccactttgtg atgagacctc	tgtcgagtgt	780
agaatacagt cactgattcc acttcgtcca gctgagcgag gaggttgcaa	gtgcacttgc	840
ggaactcctc cccgtatggt ctcagctgtat cgaagagcat	acgccttcaag acctcaaggc	900
gagccctcag gegaagcggc tcgacagtgt gagettgcgc cactactgtg	agaaggaact	960
aaacttgcct gctgttctcg gcgttagcaaa ccagatcaca cgcgcctcgc	tcggtgtgga	1020
agcccacgag atcagcatgc ttttctcac cgactacatc aagagtgc	ccggcttcag	1080
taatattttc teggacaaga aagacggcg	gcaagtatatg cgatcaaaa caggtgcgtg	1140
tgggtgcgtc tcaggtgggg gactcgttc tcaagtggtc atttcaggt	atgcgtcgat	1200
ttgccatgcc atgtcaaaagg aacttggtcc agctcagtg cacctcaaca	cccccgctgc	1260
tgaaatttag cagtcggcat cggcgtgtac agtacgatcg gcctcgccg	ccgtgttcgg	1320
aagcaaaaaag gtgggtgtt cgttaccgc aaccttgtat cccacccat	tgatttcacc	1380
acctctcccc gccgagaagc aagcattggc gaaaaattct atcctggct	actatagcaa	1440
gatagtcttc gtatggaca agccgtggtg gcccgaacaa ggcttcgc	gcgttcctca	1500
atcgagctgt gacccatct catttgcag agataccacg atcgacgtcg	atcgacaatg	1560
gtccattacc tggtagtggc tcggagaccc gggacggaa	tggtccaaac agtccaagca	1620
ggtacgacaa aagtctgtct gggaccaact ccgcgcagec tacgagaacg	ccggggccca	1680
agtccccagag cccgccaacg tgctgaaat cgagtggtcg aagcagcagt	atttccaagg	1740
agctccgagc gcccgttatg ggctgaacga tctcatcaca ctgggttcgg	cgctcagaac	1800
ccggttcaag agtggcatt tcggttggaa ggagacgtct ttagttgga	aagggtatat	1860
ggaaggggcc atacgatcgg gtcaacgagg tgctgcagaa gttgtggcta	gcctggtgc	1920
agcagcatag		1930

<210> 40
 <211> 598
 <212> PRT
 <213> Exophiala spinifera

<220>
 <221> VARIANT
 <222> (216)...(216)
 <223> Kaa = Any Amino Acid

<400> 40

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro
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Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asp	Gly	Gly	Arg	Tyr	Val
					20			25				30			
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Gly	Val	Thr	Asp	Pro
					35			40				45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys

50	55	60
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr		
65	70	75
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly		80
85	90	95
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val		
100	105	110
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala		
115	120	125
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val		
130	135	140
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln		
145	150	155
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly		160
165	170	175
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn		
180	185	190
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser		
195	200	205
Arg Leu Phe Glu Arg Phe His Xaa Glu Gly Glu Leu Gln Arg Thr Thr		
210	215	220
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro		
225	230	235
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu		240
245	250	255
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp		
260	265	270
Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala		
275	280	285
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Asn		
290	295	300
Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met		
305	310	315
Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile		320
325	330	335
Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly		
340	345	350
Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser		
355	360	365
Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly		
370	375	380
Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val		
385	390	395
Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro		400
405	410	415
Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly		
420	425	430
Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu		
435	440	445
Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe		
450	455	460
Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys		
465	470	475
Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln		480
485	490	495
Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn		
500	505	510
Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp		

515	520	525
Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu		
530	535	540
Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser		
545	550	555
Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met		
565	570	575
Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala		
580	585	590
Ser Leu Val Pro Ala Ala		
595		

<210> 41
<211> 1928
<212> DNA
<213> Rhinocladiella atrovirens

<220>
<221> intron
<222> (739)...(811)

<221> intron
<222> (1134)...(1185)

<400> 41

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cacgtcgccg taggccccaa cgaggaggagg tatgogacaa tagctggaca gattggacaa	120
gacgcttcgg ccgtgacaga ccctgcctac gagaaacagg ttgccaagc attcgccaaac	180
ctgcgagctt gtcttgcgtc agttggagcc acttcaaaccg acattaccaa gctcaattac	240
tacatgtcg actacaaccc gagcaaactc accgcaattt gagatggct gaaggttacc	300
tttgccttg acaggctccc tccttgcacg ctgggtgccag tgccggccct ggcttcacct	360
gaataccctt ttgaggttga tgccacggcg ctgggttccag gacactcaac cccagacaat	420
gttgcggacg tggcgtgtgt gggcgctggc tttagccgggt tggagacggc acgaaagtc	480
caggctgccc ggctgttctg cctcggttctt gaggegatgg atcgtgtggg gggaaagact	540
ctgagcgtac aatcggttcc cggcaggacg gctatcaatg acctcgccgc tgcgtggatc	600
aatgacacgca accaaagcga agtattcaaa ttatttggaa gatttcattt ggagggcggag	660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtaaac cactacagct	720
ccttatggtg attccttggt aagcacaatt ccattttgtt atgagacctc tgcgtgtgt	780
agaatacagt cgctgactcc acatgttcca gctgagcggag gaggttgcaa gtgcactcgc	840
ggaactcctt cccgcatggt ctcagctgtat cgaagagcat agtcttgcggatcc accccaaggc	900
gagccctcaa gcgaaggcgc tcgacagtgt gagtttgcga cactactgtt agaaggatct	960
aagttgcct gctgttctcg gcgtggccaa ccagatcaca cgcgccttcgc tcgggtgttgg	1020
agcccacgag atcagcatgc ttttttcac cgactacatc aagagtgcgc cccgttccatcg	1080
taatattgtc tggataaga aagacgggtgg gcaatgtatgc cgtatcaaaa caggtgcgtg	1140
tgggttttc tcagtggag actcggttct tagtggatcat tccaggtatg cagtcgtt	1200
gccatgccat gtcaaaaggaa cttgttccag gtcagtgca cctcaacacc cccgttgcgc	1260
aaatttgagca gtcggcatcc ggctgtacag tacgatggc ctcggggcgc gtgttccgaa	1320
gtaaaaaggt ggtggtttcg ttaccgacaa ctttgtatcc caccttgata ttttccaccac	1380
ctcttcccgc cgagaaggcaa gcattggctg aaaaatccat cctggctac tatagcaaga	1440
tagtcttcgt atgggacaag ccgtgggtgc gcaacaagg cttctgggc gtccttcataat	1500
cgagctgtga ccccatctca tttgccagag ataccagcat cgaagtcgtat cggcaatgg	1560
ccattacctg tttcatggc ggagacccgg gacggaaatgt gtcggcaacag tccaaagg	1620
tacgacagaaa gtctgttctgg aaccaactcc ggcggacttca cgagaacggc gggggccaa	1680
tcccaaggcc ggcggacatgtg ctcggatcg agtgggtcgaa gcaaggatgtat ttcggaaagg	1740
cgccggacgtgt cgcttatggg ctgaactgtc tcaacacact gggttccggc ctcggaaacgc	1800
cggtcaagggt tggatatttc gttggaaacgg agacgttctt ggtttggaaa gggatatgg	1860
aaggggccat acgatcggtt cagcgaggcg ctggcagaatgt tgggttgcgtc ctgggtccag	1920
cagcatag	1928

<210> 42
 <211> 598
 <212> PRT
 <213> Rhinocladiella atrovirens

<400> 42
 Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Leu Ala Ser Pro
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 Ala Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Ala
 20 25 30
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro
 35 40 45
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr
 65 70 75 80
 Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
 85 90 95
 Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
 100 105 110
 Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Pro Phe Glu Val Asp Ala
 115 120 125
 Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
 130 135 140
 Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
 145 150 155 160
 Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
 165 170 175
 Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Ala Ile
 180 185 190
 Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
 195 200 205
 Phe Lys Leu Phe Glu Arg Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
 210 215 220
 Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro Tyr
 225 230 235 240
 Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu
 245 250 255
 Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro
 260 265 270
 Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His
 275 280 285
 Tyr Cys Glu Lys Asp Leu Ser Leu Pro Ala Val Leu Gly Val Ala Asn
 290 295 300
 Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met
 305 310 315 320
 Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile
 325 330 335
 Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly
 340 345 350
 Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser
 355 360 365
 Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly
 370 375 380
 Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val
 385 390 395 400
 Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro

405	410	415
Pro Leu Pro Ala Glu Lys Gln Ala	Leu Ala Glu Lys Ser Ile	Leu Gly
420	425	430
Tyr Tyr Ser Lys Ile Val Phe Val	Trp Asp Lys Pro Trp Trp Arg	Glu
435	440	445
Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys	Asp Pro Ile Ser Phe	
450	455	460
Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln	Trp Ser Ile Thr Cys	
465	470	475
Phe Met Val Gly Asp Pro Gly Arg Lys	Trp Ser Gln Gln Ser Lys Gln	
485	490	495
Val Arg Gln Lys Ser Val Trp Asn Gln	Leu Arg Ala Ala Tyr Glu Asn	
500	505	510
Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val	Leu Glu Ile Glu Trp	
515	520	525
Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser	Val Val Tyr Gly Leu	
530	535	540
Asn Cys Leu Asn Thr Leu Gly Ser Ala Leu Arg	Thr Pro Phe Lys Gly	
545	550	555
Val His Phe Val Gly Thr Glu Thr Ser Leu Val	Trp Lys Gly Tyr Met	
565	570	575
Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala	Ala Glu Val Val Ala	
580	585	590
Ser Leu Val Pro Ala Ala		
595		

<210> 43
<211> 1928
<212> DNA
<213> Rhinocladiella atrovirens

<220>
<221> intron
<222> (739)...(811)

<221> intron
<222> (1134)...(1186)

<400> 43

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gacgcgttcgg ccgtgacaga ccctgcctac gagaaaacagg ttgcccaagc	attcgccaac	180
ctgcgagctt gtcttgcgtc agttggagcc acttcaaacg acattaccaa	gctcaattac	240
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tttgccttgc acaggttccc tccctgcacg ctgggtgcacg tgccggccct	ggcttccact	360
gaataccctt ttgagggttga tgccacggcg ctgggttccacg gacactcaac	cccagacaat	420
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caggctgccc ggctgttctg cctcggttctt gagggatgg atcggtgtgg	ggggaaagact	540
ctgagcgatc aatcggttcc cggcaggacg actatcaatg acctcgccgc	tgcgtggatc	600
aatgacagca accaaagcga agtattcaaa ttatgtaaa gatttcattt	ggagggcgag	660
ctccagagga cgacggaaa ttcaatccat caagcacaag acggtacaac	cactacagct	720
ccttatgggtt atcccttgtt aagcacaatt ccattttgtt atgagacctc	tgttgtgtgt	780
agaatacagt cgctgactcc acatcgatcca gctgagcgag gaggttgcaa	gtgcactcg	840
ggaactccctt cccgcgttgtt ctcagctgtat cgaagagcat agtctgtt	ggacccaaaggc	900
gagccctcaa gcgaaggcgc tcgacagtgt gagcttcgcac cactactgt	agaaggatct	960
aaacttgccct gctgttgtcg gcgtggccaa ccagatcaca cgcgcctgc	tgggtgttgg	1020
agcccacgag atcagcatgt tttttctcac cgactacatc aagagtgc	ccggtgtctcag	1080
taatattgtc tcggataaga aagacgggtgg gcagttatgt cgatgc	aaaaa caggtgcgtg	1140

tgggtttctc	tcagtggag	actcgttct	tagtggtcat	tccaggtatg	cagtcgc	ttt	1200
gccatccat	gtcaaaggaa	cttggccag	gctcagtgc	cctcaacacc	cccgtcgcc	1260	
aaattgagca	gtcgccatcc	ggctgtacag	tacgatcg	ctcgccggc	gtgttccgaa	1320	
gtaaaaaggt	ggtggttctg	ttaccgacaa	ccttgtatcc	cacccgtata	ttttcaccac	1380	
ctcttcccc	cgagaagcaa	gcattggctg	aaaaatccat	cctggctac	tatagcaaga	1440	
tagtcttcgt	atgggacaag	ccgtgggtgc	gccaacaagg	cttctcg	gtctccat	1500	
cgagctgtga	ccccatctca	tttgcagag	ataccagcat	cgaagtc	cgcaatgg	1560	
ccattacctg	tttcatggtc	ggagacc	ggacggaaatgt	gtcccaacag	tccaa	1620	
tacgacagaa	gtctgtctgg	aaccaactcc	gcccggccta	cgagaacg	ccccaaag	1680	
tcccagagcc	ggccaacgtg	ctcgagatcg	agtggtcgaa	gcagcagtat	ttccaaggag	1740	
cgccgagcgc	cgtctatggg	ctgaactgtc	tcaacacact	gggttcggcg	ctcagaacgc	1800	
cgttcaaggg	tgttcatttc	gttggAACGG	agacgtctt	ggtttgaaa	gggttatatgg	1860	
aaggggccat	acgatcggt	cagcgaggcg	ctgcagaagt	tgtggctagc	ctgggtgc	1920	
cagcatag						1928	

<210> 44
 <211> 591
 <212> PRT
 <213> Rhinocladiella atrovirens

<400> 44					
Met	Ala	Leu	Ala	Pro	Ser
1				5	
Tyr					
Ala	Gly	Tyr	Ser	Tyr	Val
				20	
					25
					30
Thr	Ile	Ala	Gly	Gln	Ile
					Gly
					Asp
					Ala
					Ser
					Ala
					Val
					Thr
					Asp
					Pro
Ala	Tyr	Glu	Lys	Gln	Val
					Ala
					Gln
					Ala
					Phe
					Ala
					Asn
					Leu
					Arg
					Ala
					Cys
50				55	
					60
Leu	Ala	Ala	Val	Gly	Ala
					Thr
					Ser
					Asn
					Asp
					Ile
					Thr
					Lys
65				70	
					75
					80
Tyr	Ile	Val	Asp	Tyr	Asn
					Pro
					Ser
					Lys
					Leu
					Thr
					Ala
					Ile
					Gly
					Asp
					Gly
Leu	Lys	Ala	Thr	Phe	Ala
					Leu
					Asp
					Leu
					Pro
					Pro
					Cys
100				105	
					110
Pro	Val	Pro	Ala	Leu	Ala
				Ser	Ser
					Pro
					Glu
					Tyr
					Leu
					Phe
115				120	
					125
Thr	Ala	Leu	Val	Pro	Gly
					His
					Ser
					Thr
					Pro
					Asp
					Asn
					Val
130				135	
					140
Val	Val	Val	Gly	Ala	Gly
					Leu
					Ser
					Gly
145				150	
					155
					160
Gln	Ala	Ala	Gly	Leu	Ser
					Cys
					Leu
					Val
					Leu
					Glu
					Ala
					Met
					Asp
					Arg
					Val
165				170	
					175
Gly	Gly	Lys	'Thr	Leu	Ser
				Val	Gln
				Ser	Ser
					Gly
180				185	
					190
Asp	Leu	Gly	Ala	Ala	'Trp
					Ile
					Asn
					Asp
					Ser
					Gln
195				200	
					205
Leu	Phe	Glu	Arg	Phe	His
					Leu
					Glu
					Gly
210				215	
					220
Asn	Ser	Ile	His	Gln	Ala
					Gln
					Asp
					Gly
225				230	
					235
					240
Gly	Ser	Leu	Leu	Ser	Glu
					Gl
					U
					Ala
					Ser
					Ala
					Leu
					Glu
					Leu
245				250	
					255
Pro	Ala	Ser	Gln	Leu	Ile
					Glu
					Glu
					His
					Ser
					Leu
260				265	
					270
Ser	Pro	Gln	Ala	Lys	Gln
					Leu
					Asp
					Ser
					Val
275				280	
					285
Glu	Lys	Leu	Asn	Leu	Ala
					Val
					Gly
					Val
					Ala
					Asn
					Gln
					Ile
					Thr
					Arg

290	295	300
Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Phe Phe Leu Thr		
305	310	315
Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Val Ser Asp Lys		
325	330	335
Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Leu		
340	345	350
Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn		
355	360	365
Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg		
370	375	380
Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val Val Leu Pro Thr		
385	390	395
Leu Tyr Pro Thr Leu Ile Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln		
405	410	415
Ala Leu Ala Glu Lys Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe		
420	425	430
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu		
435	440	445
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Glu		
450	455	460
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly		
465	470	475
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp		
485	490	495
Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu		
500	505	510
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln		
515	520	525
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly		
530	535	540
Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu		
545	550	555
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly		
565	570	575
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala		
580	585	590

<210> 45
 <211> 1928
 <212> DNA
 <213> Rhinocladiella atrovirens

<220>
 <221> intron
 <222> (739)...(811)

 <221> intron
 <222> (1134)...(1185)

<400> 45
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 cacgtcgccg taggccccaa cggaggggagg tatgtgacaa tagctggaca gattggacaa 120
 gacgcttcgg ccgtgacaga ccctgcctac gagaaaacagg ttgcccaagg attccccaac 180
 ctgcgagctt gtcttgcgtgc agttggagcc acttcaaacc acattaccaa gctcaattac 240
 tacatcgctcg actacaaccc gagcaaactc accgcaattt gagatgggct gaaggctacc 300
 tttgcccttg acaggttccc tccttgcacg ctgggtgccag tgccggccct gggttccac 360
 gaataccctt ttgaggttga tgctacggcg ctgggttccag gacactcaac cccagacaat 420

gttgcggacg	tggtcgtgg	gggcgtggc	ttgagcggtt	tggagacggc	acgcaaagt	480
caggctgccg	ggctgtctg	cctcggttct	gaggcgatgg	atcgctgtgg	gggaaagact	540
ctgagcgtac	aatcggtcc	cggcaggacg	actatcaatg	acctcggcgc	tgcgtggatc	600
aatgacagca	accaaagcga	agtattcaaa	ttatggaaa	gatttcattt	ggagggcggag	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct	720
ccttatggtg	atccccgtgt	aggcacaatt	ccatcttgg	atgagacctc	tgtctgtgt	780
agaatacagt	cgctgaatcc	acatcggtcc	gctgagcgag	gaggttgc当地	gtgcactcgc	840
ggaactcctt	cccgcatgg	ctcagctgtat	cgaaagagcat	agtcttgaag	accccaaggc	900
gagccctcaa	gccaaggcgc	tcgacagctgt	gagcttcgca	cactactgt	agaaggatct	960
aaacttgcct	gttgttctcg	gcgtggcaaa	ccagatcaca	cgcgctctgc	tgcgtgtgga	1020
agccccacgag	atcagcatgc	tttttctcac	cgactacatc	aagagtgc当地	ccggctctcg	1080
taatattgtc	tccggataaga	aagacgggtgg	cgagtatatg	cgatgc当地	caggtgcgtg	1140
tggtgttctc	tcagttggag	actcggttct	tagtggtcat	tccaggtatg	cagtcgtctt	1200
gccatgccat	gtcaaaaggaa	cttggccag	gctcagtgc当地	cctcaaacacc	cccgtcgccg	1260
aaatttgc当地	gtccggcatcc	ggctgtacag	taatgtcgcc	ctcgccggc当地	gtgttccgaa	1320
gtaaaaaaggt	ggtgtttcg	ttaccgacaa	ccttgc当地	caccttgc当地	ttttcaccac	1380
ctcttcccgc	cgagaagcaa	gcattggctg	aaaaatccat	cctgggctac	tatagcaaga	1440
tagtcttcgt	atgggacaag	ctgtgggtgg	cgaaacaagg	cttctcgccg	gtcttccaaat	1500
cgagctgtga	ccccatctca	tttgc当地	ataccagcat	cgaagtgc当地	cggtatgg	1560
ccattacctg	tttcatggtc	ggagacccgg	gacggaaatg	gtccccaaacag	tccaaaggcagg	1620
tacgacagaa	gtctgtctgg	aaccaactcc	cgccgc当地	cgagaacgc当地	ggggcccaag	1680
tcccgagagcc	ggccaaacgtg	ctcgagatcg	agtggctgaa	cgacgactat	ttccaaggag	1740
cgcccgagcgc	cgtctatggg	ctgaactgtc	tcaacacact	gggttccggc当地	ctcagaacgc当地	1800
cgttcaaggg	tgttcatttc	gttggaaacgg	agacgtctt	ggtttgaaa	gggtatatgg	1860
aaggggccat	acgatcggt	cagcgaggcg	ctgcagaatg	tgtgccttagc	ctgggtccag	1920
cagcatag						1928

<210> 46
<211> 591
<212> PRT
<213> Rhinocladiella atrovirens

<400> 46
 Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Ala Ser Pro Ala
 1 5 10 15
 Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val Thr
 20 25 30
 Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro Ala
 35 40 45
 Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys Leu
 50 55 60
 Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr Tyr
 65 70 75 80
 Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly Leu
 85 90 95
 Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val Pro
 100 105 110
 Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala Thr
 115 120 125
 Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val Val
 130 135 140
 Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
 145 150 155 160
 Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
 165 170 175
 Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
 180 185 190
 Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Phe
 80

195	200	205
Lys Leu Phe Glu Arg Phe His	Leu Glu Gly Glu	Leu Gln Arg Thr Thr
210	215	220
Gly Asn Ser Ile His Gln Ala	Gln Asp Gly Thr Thr	Thr Thr Ala Pro
225	230	235
Tyr Gly Asp Ser Leu Leu Ser	Glu Glu Val Ala Ser	Ala Leu Ala Glu
245	250	255
Leu Leu Pro Ala Trp Ser Gln	Leu Ile Glu Glu His Ser	Leu Glu Asp
260	265	270
Pro Lys Ala Ser Pro Gln Ala	Lys Gln Leu Asp Ser	Val Ser Phe Ala
275	280	285
His Tyr Cys Glu Lys Asp Leu	Asn Leu Pro Ala Val	Leu Gly Val Ala
290	295	300
Asn Gln Ile Thr Arg Ala Leu	Leu Gly Val Ala His	Glu Ile Ser
305	310	315
Met Leu Phe Leu Thr Asp Tyr	Ile Lys Ser Ala Thr	Gly Leu Ser Asn
325	330	335
Ile Val Ser Asp Lys Asp Gly	Gly Gln Tyr Met Arg	Cys Lys Thr
340	345	350
Gly Met Gln Ser Leu Cys His	Ala Met Ser Lys Glu	Leu Val Pro Gly
355	360	365
Ser Val His Leu Asn Thr Pro	Val Ala Glu Ile Glu	Gln Ser Ala Ser
370	375	380
Gly Cys Thr Val Arg Ser Ala	Ser Gly Gly Val Phe	Arg Ser Lys Lys
385	390	395
Val Ser Leu Pro Thr Thr Leu	Tyr Pro Thr Leu Ile	Phe Ser Pro Leu
405	410	415
Pro Ala Glu Lys Gln Ala Leu	Ala Glu Lys Ser Ile	Gly Tyr Tyr Ser
420	425	430
Lys Ile Val Phe Val Asp Lys	Leu Trp Trp Arg Glu	Gln Gly Phe Ser
435	440	445
Gly Val Leu Gln Ser Ser	Cys Asp Pro Ile Ser	Phe Ala Arg Asp Thr
450	455	460
Ser Ile Glu Val Asp Arg Gln	Ser Ile Thr Cys Phe	Met Val Gly Asp
465	470	475
Pro Arg Lys Trp Ser Gln	Gln Ser Lys Gln Val	Arg Gln Lys Ser Val
485	490	495
Trp Asn Gln Leu Arg Ala Ala	Tyr Glu Asn Ala	Gly Ala Gln Val Pro
500	505	510
Glu Pro Ala Asn Val Leu	Glu Ile Glu Trp Ser	Lys Gln Gln Tyr Phe
515	520	525
Gln Ala Pro Ser Ala Val	Tyr Gly Leu Asn Cys	Leu Asn Thr Leu Gly
530	535	540
Ser Ala Leu Arg Thr Pro	Phe Lys Gly Val His	Phe Val Gly Thr Glu
545	550	555
Thr Ser Leu Val Trp Lys	Gly Tyr Met Glu	Gly Ala Ile Arg Ser Gly
565	570	575
Gln Arg Gly Ala Ala Glu Val	Val Pro Ser Leu Val	Pro Ala Ala
580	585	590
<210> 47		
<211> 600		
<212> PRT		
<213> Exophiala spinifera		
<400> 47		
Met Ala Leu Ala Pro Ser Tyr	Ile Asn Pro Pro	Asn Val Ala Ser Pro
1	5	10

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
 20 25 30
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
 35 40 45
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
 65 70 75 80
 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
 85 90 95
 Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
 100 105 110
 Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
 115 120 125
 Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
 130 135 140
 Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
 145 150 155 160
 Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
 165 170 175
 Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
 180 185 190
 Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
 195 200 205
 Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
 210 215 220
 Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
 225 230 235 240
 Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
 245 250 255
 Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln
 260 265 270
 Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
 275 280 285
 Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val
 290 295 300
 Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
 305 310 315 320
 Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
 325 330 335
 Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
 340 345 350
 Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
 355 360 365
 Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala
 370 375 380
 Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
 385 390 395 400
 Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
 405 410 415
 Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile
 420 425 430
 Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
 435 440 445
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
 450 455 460
 Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
 465 470 475 480

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
 485 490 495
 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
 500 505 510
 Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
 515 520 525
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
 530 535 540
 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
 545 550 555 560
 Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
 565 570 575
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
 580 585 590
 Val Ala Ser Leu Val Pro Ala Ala
 595 600

<210> 48
 <211> 1392
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteine 461

<400> 48
 aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt 48
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10 15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt 96
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 20 25 30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg 144
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat 192
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg 240
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa 288
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95

gac ggt aca aac act aca gct cct tat ggt gac tcc ttg ctg agc gag 336
 Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 100 105 110

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctc 384

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu			
115	120	125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag			432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys			
130	135	140	
cgx ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac			480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn			
145	150	155	160
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc			528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu			
165	170	175	
ggx gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc			576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile			
180	185	190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc			624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly			
195	200	205	
ggx cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc			672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala			
210	215	220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc			720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val			
225	230	235	240
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg			768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser			
245	250	255	
ggx gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc			816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr			
260	265	270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa			864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln			
275	280	285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc			912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe			
290	295	300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc			960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu			
305	310	315	320
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac			1008
Gln Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp			
325	330	335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga			1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly			
340	345	350	

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg		1104	
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp			
355	360	365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag		1152	
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu			
370	375	380	
ccg gcc aac gtg ctc gaa atc gag tgg tgg aag cag cag tat ttc caa		1200	
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln			
385	390	395	400
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt		1248	
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly			
405	410	415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag		1296	
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
420	425	430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt		1344	
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			
435	440	445	
caa cga ggt gct gca gaa gtt gtg gct acg ctg gtg cca gca gca tag		1392	
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *			
450	455	460	

<210> 49
<211> 463
<212> PRT
<213> Unknown

<220>
<223> Cys (-) APAO; removal of cysteine 461

<400> 49			
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly			
1	5	10	15
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val			
20	25	30	
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser			
35	40	45	
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn			
50	55	60	
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu			
65	70	75	80
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln			
85	90	95	
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu			
100	105	110	
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu			
115	120	125	
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys			
130	135	140	
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn			
85			

145	150	155	160
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu			
165	170	175	
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile			
180	185	190	
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly			
195	200	205	
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala			
210	215	220	
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val			
225	230	235	240
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser			
245	250	255	
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr			
260	265	270	
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln			
275	280	285	
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe			
290	295	300	
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu			
305	310	315	320
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp			
325	330	335	
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly			
340	345	350	
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp			
355	360	365	
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu			
370	375	380	
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln			
385	390	395	400
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly			
405	410	415	
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
420	425	430	
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			
435	440	445	
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
450	455	460	

<210> 50

<211> 1392

<212> DNA

<213> Unknown

<220>

<221> CDS

<222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 50

aaa gac aac gtt gcg gac gtg gta gtg gtc ggc gct ggc ttg agc ggt	48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
1	5
	10
	15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	

20	25	30	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser 35	40	45	144
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 50	55	60	192
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 65	70	75	240
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln 85	90	95	288
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag Asp Gly Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu 100	105	110	336
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu 115	120	125	384
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys 130	135	140	432
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn 145	150	155	480
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 165	170	175	528
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 180	185	190	576
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 195	200	205	624
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala 210	215	220	672
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val 225	230	235	720
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 245	250	255	768

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc		816	
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr			
260	265	270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa		864	
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln			
275	280	285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc		912	
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe			
290	295	300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc		960	
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu			
305	310	315	320
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac		1008	
Gln Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp			
325	330	335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga		1056	
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly			
340	345	350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg		1104	
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp			
355	360	365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag		1152	
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu			
370	375	380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa		1200	
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln			
385	390	395	400
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt		1248	
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly			
405	410	415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag		1296	
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
420	425	430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt		1344	
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			
435	440	445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag		1392	
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *			
450	455	460	

<210> 5i
 <211> 463
 <212> PRT
 <213> Unknown

<220>

<223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 51

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1 5 10 15
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
20 25 30
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
35 40 45
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
50 55 60
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65 70 75 80
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
85 90 95
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
100 105 110
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
115 120 125
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
130 135 140
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
145 150 155 160
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
165 170 175
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
180 185 190
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
195 200 205
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala
210 215 220
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
225 230 235 240
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
245 250 255
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
260 265 270
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
275 280 285
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
290 295 300
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305 310 315 320
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
325 330 335
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
340 345 350
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
355 360 365
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
370 375 380
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385 390 395 400
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
405 410 415
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 435 440 445
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 52
 <211> 1392
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteines 169, 359, and
 461

<400> 52

aaa gac aac gtt	gct gtc gta	gtc gtc gtc	ggc gct ggc	ttt agc ggt	48
Lys Asp Asn Val	Ala Asp Val	Val Val Val	Gly Ala Gly	Leu Ser Gly	
1	5	10	15		

ttt gag acg gca	cgc aaa gtc cag	gcc gcc ggt	ctt agc tcc	ctc gtt	96
Leu Glu Thr Ala	Arg Lys Val Gln	Ala Ala Gly	Leu Ser Ser	Leu Val	
20	25	30			

ctt gag gcg atg	gat cgt gta	ggg gga aag	act ctg	agc gta caa tcg	144
Leu Glu Ala	Met Asp Arg	Val Gly	Gly Lys	Thr Leu Ser Val Gln Ser	
35	40	45			

ggc ccc ggc agg	acg act atc aac	gac ctc ggc	gct gcg tgg	atc aat	192
Gly Pro Gly Arg	Thr Thr Ile Asn	Asp Leu Gly	Ala Ala Trp	Ile Asn	
50	55	60			

gac agc aac caa	agc gaa gta	tcc aga ttg	ttt gaa	aga ttt cat ttg	240
Asp Ser Asn Gln	Ser Glu Val	Ser Arg	Leu Phe	Glu Arg Phe His Leu	
65	70	75	80		

gag ggc gag ctc	cag agg acg	act gga aat	tca atc	cat caa gca caa	288
Glu Gly Leu Gln	Arg Thr Thr Gly	Asn Ser Ile His	Gln Ala Gln		
85	90	95			

gac ggt aca acc	act aca gct	cct tat ggt	gac tcc ttg	ctg agc gag	336
Asp Gly Thr Thr	Ala Pro Tyr	Gly Asp Ser	Leu Leu Ser	Glu	
100	105	110			

gag gtt gca agt	gca ctt gcg	gaa ctc ctc	ccc gta tgg	tct cag ctg	384
Glu Val Ala Ser	Ala Leu Ala	Glu Leu Leu	Pro Val Trp	Ser Gln Leu	
115	120	125			

atc gaa gag cat	agc ctt caa	gac ctc aag	gcg agc	cct cag gcg aag	432
Ile Glu Glu His	Ser Leu Gln	Asp Leu Lys	Ala Ser Pro	Gln Ala Lys	
130	135	140			

cgg ctc gac agt	gtg agc ttc	gct cac tac	tgt gag aag	gaa cta aac	480
Arg Leu Asp Ser	Val Ser Phe	Ala His Tyr	Cys Glu Lys	Glu Leu Asn	
145	150	155	160		

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc		528	
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu			
165	170	175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc		576	
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile			
180	185	190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc		624	
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Asp Gly			
195	200	205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc		672	
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala			
210	215	220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc		720	
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val			
225	230	235	240
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg		768	
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser			
245	250	255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc		816	
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr			
260	265	270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa		864	
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln			
275	280	285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc		912	
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe			
290	295	300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc		960	
Val Trp Asp Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu			
305	310	315	320
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac		1008	
Gln Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp			
325	330	335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga		1056	
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly			
340	345	350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg		1104	
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp			
355	360	365	
gac caa ctc arg gca gcc tac gag aac gcc ggg gcc caa gtc cca gag		1152	
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu			
370	375	380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa		1200	
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln			

385	390	395	400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 405		410		415
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu 420	425		430	1296
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly 435	440		445	1344
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala * 450	455	460		1392
 <210> 53				
<211> 463				
<212> PRT				
<213> Unknown				
 <220>				
<223> Cys (-) APAO; removal of cysteines 169, 359, and 461				
 <400> 53				
Lys Asp Asn Val Ala Asp Val Val Val Gly Ala Gly Leu Ser Gly 1 5 10 15				
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val 20 25 30				
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser 35 40 45				
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 50 55 60				
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 65 70 75 80				
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln 85 90 95				
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu 100 105 110				
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu 115 120 125				
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys 130 135 140				
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn 145 150 155 160				
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu 165 170 175				
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile 180 185 190				
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly 195 200 205				
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala 210 215 220				
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val				

225	230	235	240
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser			
245	250	255	
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr			
260	265	270	
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln			
275	280	285	
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe			
290	295	300	
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu			
305	310	315	320
Gln Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp			
325	330	335	
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly			
340	345	350	
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp			
355	360	365	
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu			
370	375	380	
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln			
385	390	395	400
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly			
405	410	415	
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
420	425	430	
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			
435	440	445	
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala			
450	455	460	

<210> 54
<211> 8
<212> PRT
<213> Unknown

<220>
<223> Artificial Sequence

<400> 54

Gly Gly Gly Ser Gly Gly Gly Ser
1 5

<210> 55
<211> 11
<212> PRT
<213> Exophilal spinifera

<400> 55

Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1 5 10